

Run on: July 9, 2002, 12:19:55 ; Search time 10.36 Seconds (without alignments) 18.687 Million cell updates/sec		OM protein - protein search, using sw model	
Copyright (c) 1993 - 2000 CompuGen Ltd.		GenCore version 4.5	
Scoring table: BLOSUM62		Searched: 1 ANVSE 5	
Sequence: US-09-759-484-3		Total number of hits satisfying chosen parameters: 105224	
Minimum DB seq length: 0		105224 seqs, 38719550 residues	
Maximum DB seq length: 2000000000		Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database : Swissprot_40.*		Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES			
Result No.	Score	Query Length	DB ID
1	22	100.0	130
2	22	100.0	202
3	22	100.0	270
4	22	100.0	343
5	22	100.0	345
6	22	100.0	345
7	22	100.0	345
8	22	100.0	345
9	22	100.0	346
10	22	100.0	346
11	22	100.0	346
12	22	100.0	379
13	22	100.0	395
14	22	100.0	523
15	22	1862	1 GSAB_PICPA
16	21	95.5	148
17	21	95.5	279
18	21	95.5	543
19	21	95.5	553
20	21	95.5	576
21	21	95.5	1995
22	19	86.4	77
23	19	86.4	90
24	19	86.4	131
25	19	86.4	140
26	19	86.4	141
27	19	86.4	161
28	19	86.4	171
29	19	86.4	171
30	19	86.4	181
31	19	86.4	183
32	19	86.4	187
33	19	86.4	200
RESULTS			
RESULT 1	ANXIL_CHICK	STANDARD;	PRT; 130 AA.
RA.	Stols Y., Horsemann N.D.;		
RT.	"The hinge region of chicken annexin I contains no site for tyrosine phosphorylation."		
RL.	FEBS Lett. 329:296-300(1993).		
CC.	-I- FUNCTION: CATALYZES PHOSPHOTIDI-BINDING PROTEIN WHICH PROMOTES MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO FOUR CALCIUM IONS WITH HIGH AFFINITY. IT SEEMS TO BIND FROM TWO TO		
CC.	-I- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.		
CC.	-I- PTM: PHOSPHORYLATED BY PROTEIN KINASE C (BY SIMILARITY).		
CC.	-I- POLYMORPHISM: IN CONTRAST TO PIGEON, CHICKEN CONTAINS NO ISOFORMS.		
CC.	-I- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.		
CC.	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC.	CC EMBL; S64931; AAB28056.2; -		
DR.	DR HSPB; P04033; 1B09.		
DR.	DR InterPro; IPR001464; Annexin.		
DR.	DR Pfam; PF00191; annexin_1.		
DR.	DR SMART; SM00335; ANX_1.		
DR.	DR PROSITE; PS00223; ANNEXIN_1.		
DR.	DR Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation; KW		
DR.	DR Phospholipase A2 inhibitor.		
FT.	FT REPEAT 46 106 ANNEXIN_1.		
FT.	FT REPEAT 118 >130 ANNEXIN_2.		
FT.	FT MOD_RES 19 19 INTERCHAIN CROSS-LINK (BY SIMILARITY).		
FT.	FT MOD_RES 24 24 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).		
FT.	FT NON_TER 130 130 PUNTA TORMO		
SO.	SO SEQUENCE FROM N.A.		
RC.	RC TISSUE=Liver;		
RC.	RC MEDLINE=93374034; Pubmed=8365470;		
ALIGNMENTS			

Query Match		100.0%; Score 22; DB 1; Length 130;	
Best Local Similarity		100.0%; Pred. No. 13; Mismatches 0; Indels 0; Gaps 0;	
Matches		5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 AMVSE 5	1111	Db
	2 AMVSE 6	1111	
Qy	1 AMVSE 5	1111	Db
	2 AMVSE 122	1111	
RESULT 2 BIN3_STAAU STANDARD; PRT; 202 AA. ID BIN3_STAAU AC P20384; DT 01-FEB-1991 (Rel. 17, Created) DT 01-NOV-1995 (Rel. 32, Last sequence update) DT 01-NOV-1995 (Rel. 32, Last annotation update) DE Potential DNA-Invertase BIN3 (Transposon TN552). GN BIN3 OC Bacterium: Proteobacteria, gamma subdivision; Pasteurellaceae; OC Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae). OC Actinobacillus. OX NCBI_TaxID=715; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=NCTC 9189; RX MEDLINE=90060039; PubMed=2555186; OC Bacterium; Firmicutes; Bacillus/Clostridium group; OC Bacillus/Staphylococcus group; Staphylococcus. OC NCBI_TaxID=1280; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=NCTC 9189; RX MEDLINE=98013059; PubMed=9353010; OC BOSSE J.T., MacInnes J.I.; OC "Genetic and biochemical analyses of <i>Actinobacillus pleuropneumoniae</i> urease.", OC Infect. Immun. 65:4389-4394 (1997). RN Rowland S.J., Dyke K.G.H.; RN Tn552; RN [2] RP REVISIONS TO C-TERMINUS. RN STRAIN=NCTC 9189; RN Rowland S.J.; RN Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases. RN [1] RP -!- FUNCTION: BELONGS TO THE "RESOLVASE" FAMILY OF SITE-SPECIFIC RECOMBINASES. RN [2] CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). CC EMBL; U08957; AAC00065.1; -. CC InterPro; IPR002669; Ured. CC Pfam; PF01774; Ured; 1. DR EMBL; U08957; AAC00065.1; -. DR InterPro; IPR002669; Ured. DR Pfam; PF01774; Ured; 1. KW Nickel. SQ SEQUENCE 270 AA; 30215 MW; DE8C7F51D256B4B6 CRC64; 	RESULT 3 URED_AC1PL STANDARD; PRT; 270 AA. ID URED_AC1PL AC 054425; DT 15-DEC-1998 (Rel. 37, Created) DT 15-DEC-1998 (Rel. 37, Last sequence update) DT 30-MAY-2000 (Rel. 39, Last annotation update) DE Uredase accessory protein ured. GN URED. OC Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae). OC Bacterium; Proteobacteria, gamma subdivision; Pasteurellaceae; OC Actinobacillus. OX NCBI_TaxID=715; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=NCTC 9189; RX MEDLINE=98013059; PubMed=9353010; OC BOSSE J.T., MacInnes J.I.; OC "Genetic and biochemical analyses of <i>Actinobacillus pleuropneumoniae</i> urease.", OC Infect. Immun. 65:4389-4394 (1997). RN Rowland S.J., Dyke K.G.H.; RN Tn552; RN [2] RP REVISIONS TO C-TERMINUS. RN STRAIN=NCTC 9189; RN Rowland S.J.; RN Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases. RN [1] RP -!- FUNCTION: BELONGS TO THE "RESOLVASE" FAMILY OF SITE-SPECIFIC RECOMBINASES. RN [2] CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). CC EMBL; U08957; AAC00065.1; -. CC InterPro; IPR002669; Ured. CC Pfam; PF01774; Ured; 1. DR EMBL; U08957; AAC00065.1; -. DR InterPro; IPR002669; Ured. DR Pfam; PF01774; Ured; 1. KW Nickel. SQ SEQUENCE 270 AA; 30215 MW; DE8C7F51D256B4B6 CRC64; 		
RESULT 4 AN12_COLLI STANDARD; PRT; 343 AA. ID AN12_COLLI AC 092010; 092041; DT 01-NOV-1997 (Rel. 35, Created) DT 16-OCT-2001 (Rel. 40, Last sequence update) DT Annexin I, Isoform P37 (Lipocortin I) (Calpastatin 9) DE (Phospholipase A2 inhibitory protein). GN CP37. OS Columba livia (Domestic Pigeon). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Archosauvia; Aves; Neognathae; Columbiformes; Columbidae; Columba. OC NCBI_TaxID=8932; RN [1] RP SEQUENCE FROM N.A., AND SEQUENCE OF 13-50. RC STRAIN=WHITE CARNEAU; TISSUE=Crop;ac; RX MEDLINE=92406850; PubMed=1388165; RA Haigler H.T., Mangili J.A., Gao Y., Jones J., Horsemann N.D.; RT "Identification and characterization of columbid annexin Icp37." RT Insights into the evolution of annexin I phosphorylation sites."; RL J. Biol. Chem. 267:19123-19129(1992). RN [2] 	RESULT 4 AN12_COLLI STANDARD; PRT; 343 AA. ID AN12_COLLI AC 092010; 092041; DT 01-NOV-1997 (Rel. 35, Created) DT 16-OCT-2001 (Rel. 40, Last sequence update) DT Annexin I, Isoform P37 (Lipocortin I) (Calpastatin 9) DE (Phospholipase A2 inhibitory protein). GN CP37. OS Columba livia (Domestic Pigeon). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Archosauvia; Aves; Neognathae; Columbiformes; Columbidae; Columba. OC NCBI_TaxID=8932; RN [1] RP SEQUENCE FROM N.A., AND SEQUENCE OF 13-50. RC STRAIN=WHITE CARNEAU; TISSUE=Crop;ac; RX MEDLINE=92406850; PubMed=1388165; RA Haigler H.T., Mangili J.A., Gao Y., Jones J., Horsemann N.D.; RT "Identification and characterization of columbid annexin Icp37." RT Insights into the evolution of annexin I phosphorylation sites."; RL J. Biol. Chem. 267:19123-19129(1992). RN [2] 		

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CC DR EMBL; X05908; CAA29338.1; -.

CC DR PIR; A03080; LUHU.

CC DR PIR; S2246; S28846.

CC DR PDB; 1AIN; 15-JUL-93.

CC DR PDB; 1B09; 19-AUG-98.

CC DR PHCI-DPAGE; P04083; -.

CC DR MIM; 151690; -.

CC DR InterPro; IPR001464; Annexin.

CC DR Pfam; PF00191; annexin; 4.

CC DR PRINTS; PRO00196; ANNEXIN.

CC DR SMART; SM00335; ANX; 4.

CC DR PROSITE; PS00223; ANNEXIN; 4.

CC KW Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure;

CC KW Phospholipase A2 inhibitor; Phosphorylation; Acetylation.

CC FT INIT-MET 0 0

CC FT REPEAT 50 110

CC FT REPEAT 122 182

CC FT REPEAT 206 266

CC FT REPEAT 281 341

CC FT MOD-RES 1 1

CC FT MOD-RES 18 18

CC FT MOD-RES 20 20

CC FT MOD-RES 23 23

CC FT MOD-RES 26 26

CC SQ SEQUENCE 345 AA; 38583 MW; 90A245C9E69F5011 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 345;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMVSE 5

Db 1 AMVSE 5

RESULT 6

ANXL_MOUSE ID ANXL_MOUSE STANDARD; PRT; 345 AA.

AC P10107; DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 15-OCT-2001 (Rel. 40, Last annotation update)

DE Annexin I (Lipoprotein I) (Calmodulin II) (Chromobindin 9) (P35)

DE (Phospholipase A2 inhibitory protein).

GN ANXA1 OR ANX1 OR LPLC1 OR LPC1-1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus. OX NCBL-TaxID=10090; RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DS;

RX MEDLINE=89165848; PubMed=2522299;

RX PIR; S2246; S28846.

RX SEQUENCE FROM N.A.

RX MEDLINE=91301652; PubMed=1675980;

RX "Mouse lipocortin I gene structure and chromosomal assignment: gene duplication and the origins of a gene family.";

RX Genomics 10:365-374(1991).

RN [3]

SEQUENCE OF 5-345 FROM N.A.

Query Match 100.0%; Score 22; DB 1; Length 345;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMVSE 5

Db 1 AMVSE 5

RESULT 7

RX MEDLINE=89165848; PubMed=2522299;

RA Philips C., Rose-John S., Rincke G., Fuerstenberger G., Marks F.;

RT "cDNA-cloning, sequencing and expression in glucocorticoid-stimulated quiescent Swiss 3T3 fibroblasts of mouse lipocortin I.";

RT Biochem. Biophys. Res. Commun. 159:155-162(1989).

CC -!- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEKS TO BIND FROM TWO TO FOUR CALCIUM IONS WITH HIGH AFFINITY.

CC -!- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.

CC -!- PFM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE INHIBITORY ACTIVITY (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

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CC DR EMBL; X07486; CAA0371.1; -.

CC DR EMBL; M69260; AAA39437.1; -.

CC DR EMBL; M69250; AAA39437.1; JOINED.

CC DR EMBL; M69251; AAA39437.1; JOINED.

CC DR EMBL; M69252; AAA39437.1; JOINED.

CC DR EMBL; M69253; AAA39437.1; JOINED.

CC DR EMBL; M69254; AAA39437.1; JOINED.

CC DR EMBL; M69255; AAA39437.1; JOINED.

CC DR EMBL; M69256; AAA39437.1; JOINED.

CC DR EMBL; M69257; AAA39437.1; JOINED.

CC DR EMBL; M69258; AAA39437.1; JOINED.

CC DR EMBL; M69259; AAA39437.1; JOINED.

CC DR EMBL; M24554; AAA39420.1; -.

CC DR PIR; S0281; LUNSI.

CC DR HSSP; P04083; 1B09.

CC DR MGII:96819; Anxal.

CC DR InterPro; IPR001464; Annexin.

CC DR Pfam; PF00191; annexin; 4.

CC DR PRINTS; PRO00196; ANNEXIN.

CC DR SMART; SM00335; ANX; 4.

CC DR PROSITE; PS00223; ANNEXIN; 4.

CC KW Annexin; Calcium/phospholipid-binding; Repeat;

CC KW Phospholipase A2 inhibitor; Phosphorylation.

CC FT INIT-MET 0 0

CC FT REPEAT 50 110

CC FT REPEAT 122 182

CC FT REPEAT 206 266

CC FT REPEAT 281 341

CC FT MOD-RES 18 18

CC FT MOD-RES 20 20

CC FT MOD-RES 26 26

CC FT CONFLICT 77 78

CC FT CONFLICT 211 211

CC FT CONFLICT 221 221

CC FT CONFLICT 273 273

CC SQ SEQUENCE 345 AA; 38603 MW; 1785ACACDB691C3ED CRC64;

CC -!- PWM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE INHIBITORY ACTIVITY (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

CC -----

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CC -----

CC EMBL; X95108; CAA64477.1; -.

DR PIR; A26188; A26188.

DR PDB; 1HMG; 28-FEB-01.

DR InterPro; IPR004646; Annexin.

DR Pfam; PF00191; annexin; 4.

DR SMART; SM00335; ANX; 4.

DR PROSITE; PS00223; ANNEXIN; 3.

KW Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;

KW Phospholipase A2 inhibitor; Phosphorylation; 3D-structure.

FT REPEAT 51 111; ANNEXIN 1.

FT REPEAT 123 183; ANNEXIN 2.

FT REPEAT 207 367; ANNEXIN 3.

FT REPEAT 282 342; ANNEXIN 4.

FT MOD_RES 19 19; INTERCHAIN CROSS-LINK (BY SIMILARITY).

FT MOD_RES 21 21; PHOSPHORYLATION (BY EGFR).

FT MOD_RES 24 24; PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

FT MOD_RES 41 41; T -> S (IN REF. 2).

FT SEQUENCE 346 AA; 38759 MW; 925845C5D8BCB82 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 346; Best Local Similarity 100.0%; Pred. No. 38; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AMVSE 5

Db 2 AMVSE 6

RESULT 11

ID ANX1_RABBIT STANDARD; PRT; 346 AA.

AC P51662;

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Annexin I (Lipocartin I) (Calpactin II) (Chromobindin 9) (P35) (Phospholipase A2 inhibitory protein).

DE DE

GN ANX1 OR ANX1.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OC NCBI_TaxID=986;

RN [1]

RP SEQUENCE FROM N.A.

RT TISSUE-LUNG;

RA Tsao F-H-C, Wen C, Hu J;

RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS. THIS PROTEIN REGULATES PHOSPHOLIPASE A2 ACTIVITY. IT SEEMS TO BIND FROM TWO TO FOUR CALCIUM IONS WITH HIGH AFFINITY.

CC -!- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.

CC -!- PWM: PHOSPHORYLATED BY PROTEIN KINASE C AND EPIDERMAL GROWTH FACTOR RECEPTOR/KINASE. PHOSPHORYLATION RESULTS IN LOSS OF THE INHIBITORY ACTIVITY (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

CC -----

CC EMBL; X95108; CAA64477.1; -.

DR PIR; A26188; A26188.

DR PDB; 1HMG; 28-FEB-01.

DR InterPro; IPR004646; Annexin.

DR Pfam; PF00191; annexin; 4.

DR SMART; SM00335; ANX; 4.

DR PROSITE; PS00223; ANNEXIN; 3.

KW Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;

KW Phospholipase A2 inhibitor.

FT REPEAT 51 111; ANNEXIN 1.

FT REPEAT 123 183; ANNEXIN 2.

FT REPEAT 207 267; ANNEXIN 3.

FT REPEAT 282 342; ANNEXIN 4.

FT MOD_RES 19 19; INTERCHAIN CROSS-LINK (BY SIMILARITY).

FT MOD_RES 21 21; PHOSPHORYLATION (BY EGFR) (BY SIMILARITY).

FT MOD_RES 27 27; PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

FT SEQUENCE 346 AA; 38735 MW; 64EEBAF889D06A3D CRC64;

Query Match 100.0%; Score 22; DB 1; Length 346; Best Local Similarity 100.0%; Pred. No. 38; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AMVSE 5

Db 2 AMVSE 6

RESULT 12

ID HYPD_ALCEU STANDARD; PRT; 379 AA.

AC P11903;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUL-1993 (Rel. 38, Last annotation update)

DE Hydrolase expression/protein hypd.

GN HYPD.

OS Alcaligenes eutrophus (Ralstonia eutropha).

OC Plasmid megaplasmid ph01.

OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;

OC Ralstonia.

OC NEBIL_TaxID=510;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-H16 / ATCC 17699;

RX MEDLINE:9335697; PubMed=8352644;

RA Dermedde J, Eitinger M, Friedrich B;

RT Analysis of a plieotrophic gene region involved in formation of catalytically active hydroxogenases in Alcaligenes eutrophus H16.;"

RL Arch. Microbiol. 159:545-553(1993)

CC -!- SIMILARITY: BELONGS TO THE H16 FAMILY.

CC -----

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CC -----

CC EMBL; U24656; AAC78495.1; -.

DR HSSP; P04083; IBO9.

DR InterPro; IPR00164; Annexin.

DR Pfam; PF00191; annexin; 4.

DR PRINTS; PR00196; ANNEXIN.

DR SMART; SM00335; ANX; 4.

DR PROSITE; PS00223; ANNEXIN; 3.

KW Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;

KW Phospholipase A2 inhibitor.

FT REPEAT 51 111; ANNEXIN 1.

FT REPEAT 123 183; ANNEXIN 2.

FT REPEAT 207 267; ANNEXIN 3.

FT REPEAT 282 342; ANNEXIN 4.

FT MOD_RES 19 19; INTERCHAIN CROSS-LINK (BY SIMILARITY).

FT MOD_RES 21 21; PHOSPHORYLATION (BY EGFR) (BY SIMILARITY).

FT MOD_RES 27 27; PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

FT SEQUENCE 346 AA; 38735 MW; 64EEBAF889D06A3D CRC64;

Query Match 100.0%; Score 22; DB 1; Length 346; Best Local Similarity 100.0%; Pred. No. 38; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AMVSE 5

Db 2 AMVSE 6

RESULT 12

ID HYPD_ALCEU STANDARD; PRT; 379 AA.

AC P11903;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUL-1993 (Rel. 38, Last annotation update)

DE Hydrolase expression/protein hypd.

GN HYPD.

OS Alcaligenes eutrophus (Ralstonia eutropha).

OC Plasmid megaplasmid ph01.

OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;

OC Ralstonia.

OC NEBIL_TaxID=510;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-H16 / ATCC 17699;

RX MEDLINE:9335697; PubMed=8352644;

RA Dermedde J, Eitinger M, Friedrich B;

RT Analysis of a plieotrophic gene region involved in formation of catalytically active hydroxogenases in Alcaligenes eutrophus H16.;"

RL Arch. Microbiol. 159:545-553(1993)

CC -!- SIMILARITY: BELONGS TO THE H16 FAMILY.

CC -----

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CC -----

CC EMBL; X70183; CAA49734.1; -.

DR PIR; S29978; S29978.

DR InterPro; IPR002780; HYPD.

DR Pfam; PF01924; HYPD; 1.

KW Metal-binding; Plasmid.
FT POTENTIAL.
FT METAL
FT 64
FT 67
FT METAL
FT 67
FT POTENTIAL.
SEQUENCE 379 AA; 41907 MW; 510401FAA6AB224 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 395;
Best Local Similarity 100.0%; Pred. No. 41; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMVE 5
Db 270 AMVE 274

RESULT 13
NH10_CAEL STANDARD; **PRT**; 395 AA.
ID NH10_CAEL
AC P41999
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Nuclear hormone receptor family member nrh-10.
GN NHR-10 OR B0280.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peioderinae; Caenorhabditis.
OX NCBI_TaxID=6239;

RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Ralton L.; Waterston R.;
RL Submitted (JUN 1994) to the EMBL/GenBank/DBJ databases.
CC !-- FUNCTION: ORPHAN NUCLEAR RECEPTOR.
CC !-- SUBCELLULAR LOCATION: NUCLEAR (Potential).
CC !-- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.

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CC !-- DOMAIN BELONGS TO THE SRC SUBFAMILY.

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DR EMBL: 010438; AAA19086.1; -.
DR HSSP: P19793; 2NLL.
DR WormPep: B0280.8; CE00815.
DR InterPro: IPR00536; Hormone_rec_lig.
DR InterPro: IPR001628; zf-C4.
DR Pfam: PF00104; hormone_rec; 1.
DR Pfam: PF00105; zf-C4; 1.
DR PRINTS: PRQ0047; STRODIFINGER.
DR SMART: SM00430; HOLT; 1.
DR SMART: SM00399; ZnF_C4; 1.
DR PROSITE: PS00031; NUCLEAR RECEPTOR; 1.
DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
DR Zinc-finger.
FT DNA_BIND; 18
FT ZN_FING; 18
FT ZN_FING; 54
FT SEQUENCE 395 AA; 44899 MW; AFDB075D989EEBEA CRC64;

Query Match 100.0%; Score 22; DB 1; Length 395;
Best Local Similarity 100.0%; Pred. No. 43; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMVE 5
Db 119 AMVE 123

RESULT 14
SRCS_RVPA STANDARD; **PRT**; 523 AA.
ID SRCS_RVPA
AC P31633
DT 01-JUL-1993 (Rel. 25, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE Tyrosine protein kinase transforming protein SRC (EC 2.7.1.112) (P60-
DE SRC).
GN V-SRC.
OS Rous sarcoma virus (strain PA101).
OC Viruses; Retrovirus; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=31677;
RN [1]
SEQUENCE FROM N.A.
CC MEDLINE=9235154; PubMed=1322589;
RA Dezelie P.; Barnier J.V.; Hampe A.; Laugier D.; Marx M.; Galibert F.;
RA Calotry G.;
CC "Small deletion in v-src SH3 domain of a transformation defective
RT mutant of Rous sarcoma virus restores wild type transforming
RT properties";
RL Virology 189:556-567 (1992).
CC !-- FUNCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION
CC AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN
CC KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
CC IN VITRO.
CC !-- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC !-- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC !-- SIMILARITY: BELONGS TO THE SRC SUBFAMILY.

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DR EMBL: M84475; AAA42581.1; ALT_SEQ.
DR PIR: A42934; PIRMT.
DR HSSP: P00524; ISPS.
DR InterPro: IPR00719; Euk_pk kinase.
DR InterPro: IPR00980; SH2.
DR InterPro: IPR01452; SH3.
DR InterPro: IPR01245; Tyr_pk kinase.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PRQ0041; SH2DOMAIN.
DR PRINTS: PRQ0109; TYRINKASE.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TYRk; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50022; SH3; 1.
DR PROSITE: PS50017; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50019; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50001; SH2; 1.
DR KW Tyrosine-protein kinase; Oncogene; Transferase; Phosphorylation;
KW ATP-binding; Myristate; SH3 domain; SH2 domain.
FT DOMAIN 145 242 SH2.
FT DOMAIN 75 139 SH3.
FT DOMAIN 2 2 SH3.
FT DOMAIN 264 514 PROTEIN KINASE.
FT DOMAIN 270 278 ATP (BY SIMILARITY).
FT BINDING 292 292 ATP (BY SIMILARITY).
FT ACT_SITE 383 383 BY SIMILARITY.
FT MOD_RES 413 413 PHOSPHORYLATION (AUTO-).
SQ SEQUENCE 523 AA; 58778 MW; 853245739f6b909ed CRC64;

Query Match 100.0%; Score 22; DB 1; Length 523;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AMVSE 5
 Db 324 AMVSE 328

RESULT 15
 GSAB_PICPA STANDARD;
 ID GSAB_PICPA PRT; 1862 AA.
 AC 09HE34;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Pexophagy regulatory protein Gsall.
 DE Gsall.
 OS Pichia pastoris (yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TAXID=4922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=11551190; PubMed=11533052;
 RA Stromhaug P.E., Bevan A., Dunn W.A. Jr.;
 RT "Gsall encodes a unique 208 kDa protein required for pexophagy and
 autophagy in *Pichia pastoris*";
 RL J. Biol. Chem. 276:42422-42435 (2001).
 CC -!- FUNCTION: REQUIRED FOR GLUCOSE-INDUCED PEROXISOME AUTOPHAGY
 CC (PEXOPHAGY).
 CC -!- SUBCELLULAR LOCATION: Nuclear (BY SIMILARITY).
 CC -!- SIMILARITY: CONTAINS 1 ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR
 CC CLUSTER DOMAIN
 CC
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 DR EMBL; AF309871; AAG30392.1;
 DR InterPro; IPR001138; Zn2_Cy6_fungal.
 DR Pfam; PF00172; Zn_Clus; 1.
 DR SMART; SM00066; GAL4; 1.
 DR PROSITE; PS0048; ZN2_CY6_FUNGAL_2; 1.
 KW Transcription regulation; Activator; DNA-binding; Nuclear protein;
 KW Zinc; Metal-binding; Autophagy;
 FT DNA_BIND; 632 659
 SEQUENCE 1862 AA; 208595 MW; 1CC87BEC1FA21EF8 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 1862;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMVSE 5
 Db 447 AMVSE 451

Search completed: July 9, 2002, 12:23:20
 Job time: 205 sec

